

**Fig. 1a**

**MET\_T9 (SEQ ID NO: 3)**

gaatttcgcgcctcgccgcccgcggcgccccgagcgctttgtgagcagatgcgggagccgag  
tggagggcgcgagccagatgcggggcgacagctgacttgctgagaggaggcggggaggcg  
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tcattaaagctcatttatgtgtgggttttgggtcatcaactc

**Fig. 1b**

**MET T9 (SEQ ID NO: 1)**

MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHE  
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ALVVDTTYDDQLISCGSVNRGTCQRHVFPNHTADIQSEVHCIFSPQIEEPSQCPDCVV  
SALGAKVLSSVKDRFINFFVGNTINSSYFPDHPLHSISVRRLKETKDGMFLTDQSYID  
VLPEFRDSYPIKYVHAFESNNFIYFLTQVRETLDQTFHTRIIRFCSINSGLHSYMEMP  
LECILTEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQSKPDSA  
EPMDRSAMCAFPKIYVNDFFNKIVNKNVRLQHFYGPNEHC FNRTLLRNSSGCEARR  
DEYRTEFTTALQVRDLFMGQFSEVLLTSISTFIKGLTIANLGTSEGRFMQVVVSRSGP  
STPHVNFLLD SHPVSPEVIVEHTLNQNGYTLVITGKKITKIPLNGLGCRHFQSCSQCLS  
APPFVQCGWCHDKCVRSEEC LSGTWTQQICLPAIYKVFPNSAPLEGGTRLTICGWDFGF  
RRNNKFDLKKTRVLLGNESCTLT LSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTQY  
STFSYVDPVITSISP KYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLKSVSNSILE  
CYTPAQTISTEFAVKLKIDLANRETSIFS YREDPIVYEIHPTKSFISGGSTITGVGKNL  
NSVSVPRMVINVEAGRNF TVACQHRNSNEIICCTTPSLQQLNLQLPLKTKAFFMLDGI  
LSKYFDLIYVHNPFVKPF EKPVMSMGNE NVLEIKGNDIDPEAVKGEVLKVG NKSCENI  
HLHSEAVLCTVPNDLLKL NSELNIEVGFLHSSHDVNKEASVIMLF SGLK

**Fig. 3 (page 1/2)**

hsu08818\_t9.pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:MET\_HUMAN

Sequence documentation:

Hepatocyte growth factor receptor precursor (EC 2.7.1.112) (Met proto- oncogene tyrosine kinase) (c-met) (HGF receptor) (HGF-SF receptor). Homo sapiens (Human). P08581; O60366; Q9UPL8;

Alignment of: HSU08818\_T9 x MET\_HUMAN ..

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      1 MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAET 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAET 50

     51 PIQNVILHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFCPCQD 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
     51 PIQNVILHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFCPCQD 100

    101 CSSKANLSGGVWKDNINMALVVDITYDDQLISCGSVNRGTCQRHVFPNH 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
    101 CSSKANLSGGVWKDNINMALVVDITYDDQLISCGSVNRGTCQRHVFPNH 150

    151 TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGNT 200
      ||||||||||||||||||||||||||||||||||||||||||||||||
    151 TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGNT 200

    201 INSSYFPDHPLHSISVRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV 250
      ||||||||||||||||||||||||||||||||||||||||||||||||
    201 INSSYFPDHPLHSISVRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV 250

    251 HAFESNNFIYFLTVQRETLDQTFHTRIIRFCSINSGLHSEMPLECIL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||
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    301 TEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQSK 350

    351 PDSAEPMDRSAMCAFPKIYVNDFFNKIVNKNVRCLOHFYGPNEHCENR 400
      ||||||||||||||||||||||||||||||||||||||||||||||||
    351 PDSAEPMDRSAMCAFPKIYVNDFFNKIVNKNVRCLOHFYGPNEHCENR 400

    401 TLLRNSSGCEARRDEYRTEFTTALQRVDFMGQFSEVLLTSISTFIKGD 450
      ||||||||||||||||||||||||||||||||||||||||||||||||
    401 TLLRNSSGCEARRDEYRTEFTTALQRVDFMGQFSEVLLTSISTFIKGD 450

    451 TIANLGTSEGRFMQVVVSRSRGPSTPHVNFLDSDHPVSPEVIVEHTLNQ 500
      ||||||||||||||||||||||||||||||||||||||||||||||||
    451 TIANLGTSEGRFMQVVVSRSRGPSTPHVNFLDSDHPVSPEVIVEHTLNQ 500

    501 YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDKCVRSE 550
      ||||||||||||||||||||||||||||||||||||||||||||||||
    501 YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDKCVRSE 550

    551 CLSGTWTQQICLPAIYKVFNSAPLEGGTRLTICGWDFGFRNNKFDLKK 600
      ||||||||||||||||||||||||||||||||||||||||||||||||
    551 CLSGTWTQQICLPAIYKVFNSAPLEGGTRLTICGWDFGFRNNKFDLKK 600
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Fig. 3 (page 2/2)

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601 TRVLLGNESCTLTLESTMTNLTCTVGPAMNKHFNMSIIISNGHGTQYS 650
    ||||||||||||||||||||||||||||||||||||||||||||
601 TRVLLGNESCTLTLESTMTNLTCTVGPAMNKHFNMSIIISNGHGTQYS 650

651 TFSYVDPVITSISP KYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLK 700
    ||||||||||||||||||||||||||||||||||||||||||||
651 TFSYVDPVITSISP KYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLK 700

701 SVSNSILECYTPAQTI STEFAVKLKIDLANRETSIFS YREDPIVYEIHPT 750
    ||||||||||||||||||||||||||||||||||||||||||||
701 SVSNSILECYTPAQTI STEFAVKLKIDLANRETSIFS YREDPIVYEIHPT 750

751 KSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNF TVACQHRNSEIIC 800
    ||||||||||||||||||||||||||||||||||||||||||||
751 KSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNF TVACQHRNSEIIC 800

801 CTTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPF EKPVMI 850
    ||||||||||||||||||||||||||||||||||||||||||||
801 CTTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPF EKPVMI 850

851 SMGNENVLEIKGNDIDPEAVKGEVLKVG NKSCENIHLHSEAVLCTVPNDL 900
    ||||||||||||||||||||||||||||||||||||||||||||
851 SMGNENVLEIKGNDIDPEAVKGEVLKVG NKSCENIHLHSEAVLCTVPNDL 900

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    ||||||||
901 LKLNSELNIE..... 910
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# MET structure

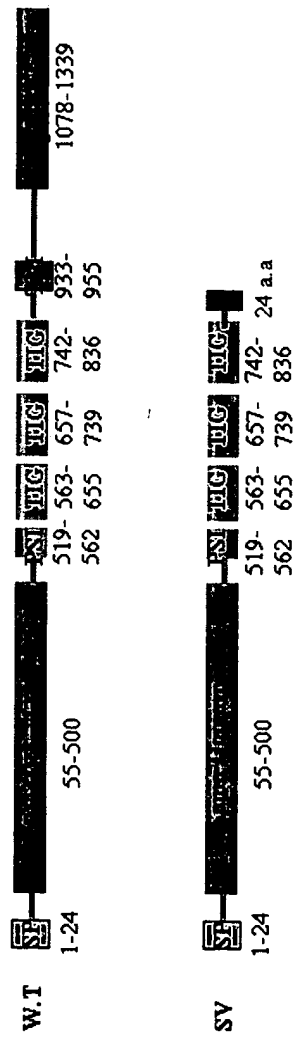


Fig. 4

**Fig. 5a**

**IL6\_T6 (SEQ ID NO: 7)**

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**Fig. 5b**

**IL-6 T6 (SEQ ID NO: 5)**

MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYI  
LDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFSQSGFNEETCLVKIITGLL  
EFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKVGVSSFPQLGVGEDRLKDSVLDN  
SGMQCHFQKRRLHVNKRV

## Interleukin 6





**Fig. 7**

s56892\_p6(t6).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL6\_HUMAN

Sequence documentation:

Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2) (Interferon beta-2) (Hybridoma growth factor) (CTL differentiation factor) (CDF). Homo sapiens (Human). P05231; Q9UCU2; Q9UCU3; Q9UCU4;

Alignment of: S56892\_P6 x IL6\_HUMAN ..

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      1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50
        ||||||||||||||||||||||||||||||||||||||||||||
      1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50

     51 ERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDG 100
        ||||||||||||||||||||||||||||||||||||||||||||
     51 ERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDG 100

    101 CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVL 150
        ||||||||||||||||||||||||||||||||||||||||||||
    101 CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVL 150

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## IL-6 structure

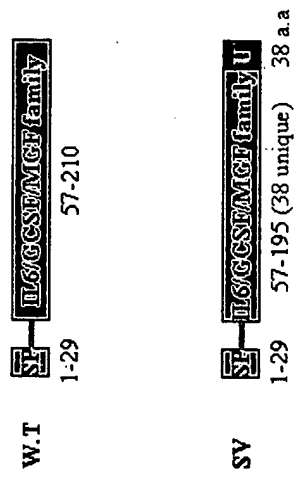


Fig. 8

**Fig. 9a**

**IL-7 T7 (SEQ ID NO: 11)**

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**Fig. 9b.**

**IL-7 T7 (SEQ ID NO: 9)**

MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDQKQYESVLMVSIQQLDSMKEIGSNCL  
NNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQ  
VKGRKPAALGEAQPTKSLSSGLQKQFTFYRSNGRHTHSFHCKLSFLH

**Fig. 9c**

**IL7-T8 (SEQ ID NO: 15)**

aagacgaatagtttgatttatttagccaattcagataaatgtgcacgtggaagtcatagtt  
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tcacaaattttcttatatttgaaataatctgattcaaatgagaactttaacctaaaactt  
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**Fig. 9d**

**IL7 T8** (SEQ ID NO: 13)

MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDQYESVLMVSIQQLDSMKEIGSNCL  
NNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQ  
VKGRKPAALGEAQPTKSLVELIIPSCMPPLLSSTSNS

FIGURE 10

Interleukin 7

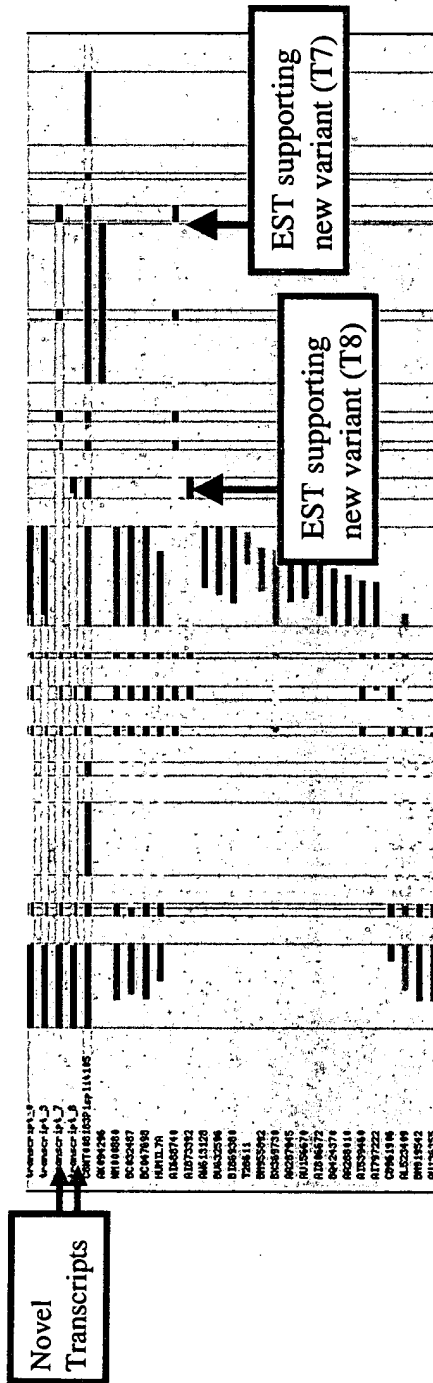


Fig. 11a

humil7a\_p4(t7).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL7\_HUMAN

Sequence documentation:

Interleukin-7 precursor (IL-7). Homo sapiens (Human). P13232;

Alignment of: HUMIL7A\_P4 x IL7\_HUMAN ..

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      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100

      101 DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSLSSGLQKQFTFYR 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
      101 DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSL..... 138

      151 SNGRHTHSFHCKLSFLH 167

      138 ..... 138
```



**Fig. 11b**

humil7a\_p5 (t8).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL7\_HUMAN

Sequence documentation:

Interleukin-7 precursor (IL-7). Homo sapiens (Human). P13232;

Alignment of: HUMIL7A\_P5 x IL7\_HUMAN ..

```

      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGKQYESVLMVSIQQLD 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGKQYESVLMVSIQQLD 50

      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100

      101 DLHLLKVSEGT TILLNCTGQVKGRKPAALGEAQPTKSLVELIIPSCMPPL 150
      ||||||||||||||||||||||||||||||||||||||||||||
      101 DLHLLKVSEGT TILLNCTGQVKGRKPAALGEAQPTKSL..... 138

      151 LSSTSNS 157

      138 ..... 138
```

# IL-7 structure



Fig. 12

Fig. 13a

TNFR9 T4 (SEQ ID NO: 19)

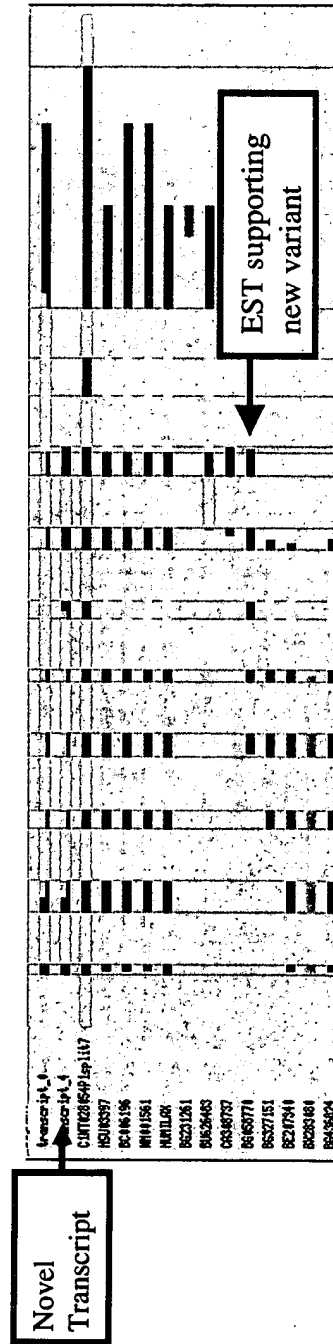
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ctcttctgtgttcttctcactcgcgttctctgttggttaaaccggggcagaaagaaa  
ctcctgtatatattcaaacacgtaagattaacataatcatattacagctctggca

**Fig. 13b**

**TNFR9 T4 (SEQ ID NO: 17)**

MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQR  
TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHLGAGCSMCEQDCKQGQELTKKGCKDC  
CFGTFNDQKRGICRPWTNIRVADEWNHDSQEKY

**FIGURE 14**  
**Tumor necrosis factor receptor-9/4-1BB**



**Fig. 15**

hsu03397\_p4 (T4).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:TNR9\_HUMAN

Sequence documentation:

Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen). Homo sapiens (Human). Q07011;

Alignment of: HSU03397\_P4 x TNR9\_HUMAN ..

```

      1 MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPP 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPP 50

      51 NSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCS 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 NSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCS 100

      101 MCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTNIRVADEWNHDSQ 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
      101 MCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTN..... 138

      151 EKY 153

      138 ... 138
```

# TNFR 9- structure

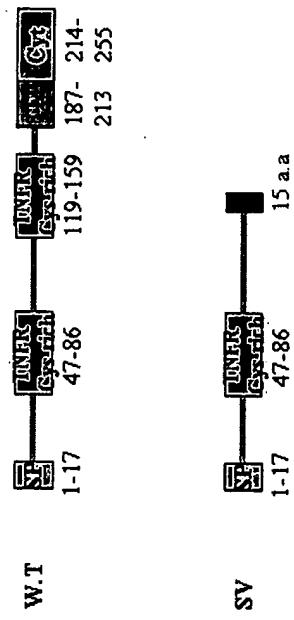


Fig. 16

Fig. 17a

IL-4R T4 (SEQ ID NO: 23)

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**Fig. 17b**

**IL-4R T4 (SEQ ID NO: 21)**

MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMGPTNCSTELR  
LLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS  
EHVLPPLKRSWSQ

**Fig. 17c**

**IL-4R T11 (SEQ ID NO: 27)**

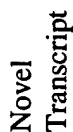
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aagtggcacaaactgtgagtatcaagagggcTAAgcaatggtaatctccactctccattcttccccctgtggccagacact  
ccccctggctgagtcctctgggc

**Fig. 18**

**IL-4R T11 (SEQ ID NO: 25)**

MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMGPTNCSTELR  
LLYQLVFLLSEHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLWKGSFKPS  
EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPDPNYLYNHLTYAVNIWSENDPADFRIYNV  
TYLEPSLRIAASTLKSGISYRARVRAWAQCYNTTWSEWSPSTKWHNCEYQEA

**FIGURE 2**



**Fig. 19a**

cds-2\_hsil4r\_t4.pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL4R\_HUMAN

Sequence documentation:

Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen). Homo sapiens (Human). P24394; Q96P01;

Alignment of: CDS-2\_HSIL4R\_T4 x IL4R\_HUMAN ..

```

      1 MGWLC SGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMN 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGWLC SGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMN 50

      51 PTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 PTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100

      101 LDLWAGQQLLWKGSFKPSEHVL PPLKRSWSQ                      131
      ||||||||||||||||||||
      101 LDLWAGQQLLWKGSFKPSEHV.....                          121
```

Fig. 19b

cds-2\_hsil4r\_t11.pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:IL4R\_HUMAN

Sequence documentation:

Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen). Homo sapiens (Human). P24394; Q96P01;

Alignment of: CDS-2\_HSIL4R\_T11 x IL4R\_HUMAN ..

```

      1 MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMNNG 50
      |||||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMNNG 50

    51 PTNCSTELRLLYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100
      |||||||||||||||||||||||||||||||||||||||||||||||||||
    51 PTNCSTELRLLYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100

   101 LDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPPD 150
      |||||||||||||||||||||||||||||||||||||||||||||||||||
   101 LDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPPD 150

   151 NYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRAR 200
      |||||||||||||||||||||||||||||||||||||||||||||||||||
   151 NYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRAR 200

   201 VRAWAQCYNNTTWSEWSPSTKWHNCEYQEA 229
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# IL4R structure

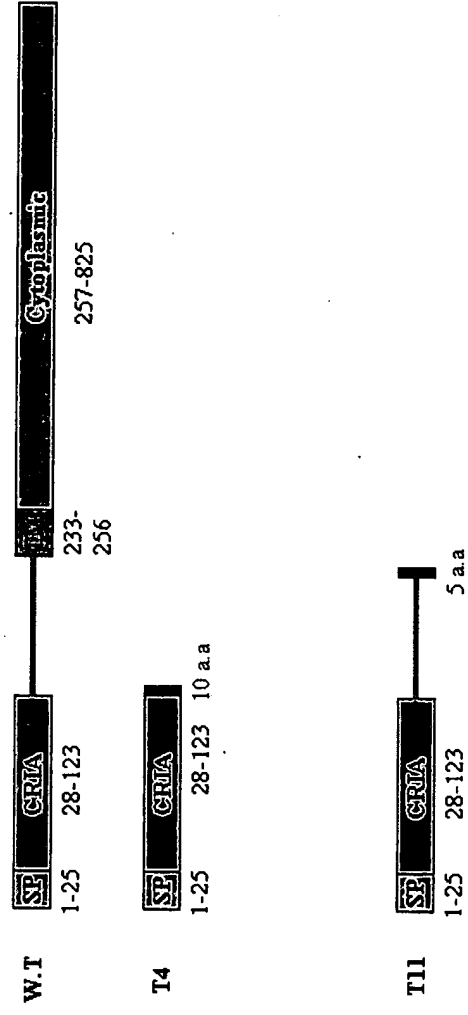


Fig. 20

**Fig. 21a**

**TGR2\_T7 (SEQ ID NO: 31)**

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aatgtgctcgcgactcaatagattggagtagttcactcctggatctcaacttgcaatttga  
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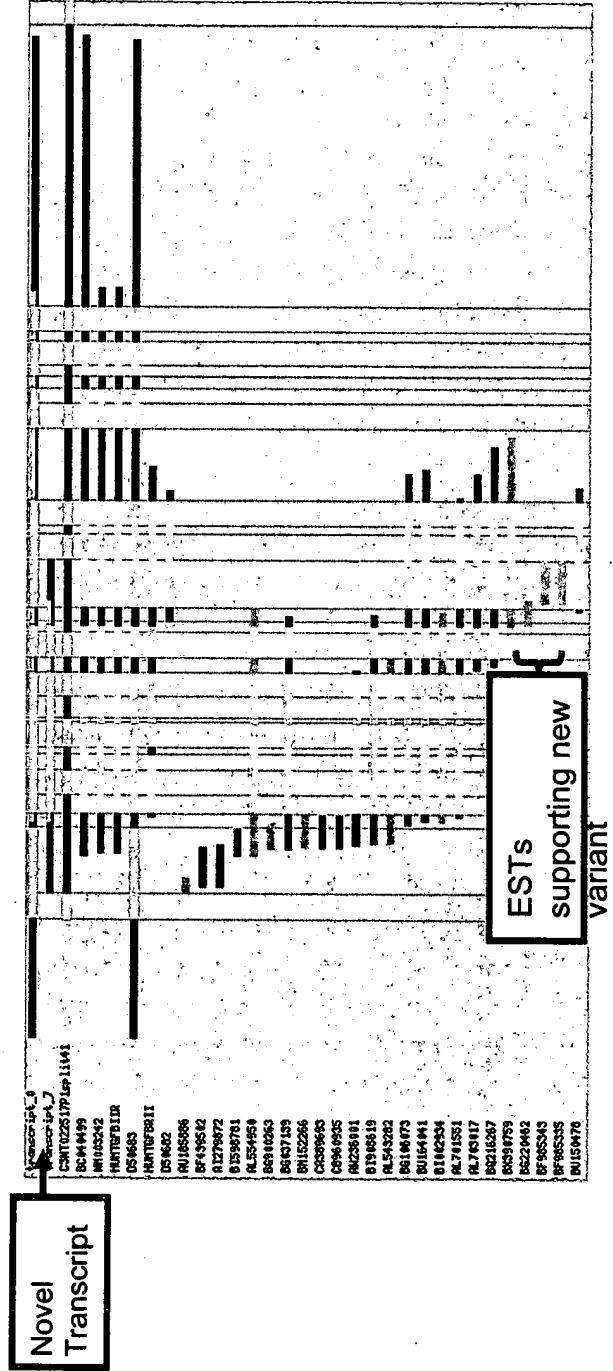


**Fig. 21b**

**TGR2\_T7 (SEQ ID NO: 29)**

MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFST  
CDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETVCHDPKLPYHDFILEDAAASP  
CIMKEKKKPGETFFMCSSDECNDNIIFSEGEFSSLKGVGPEICANFLYPWSAVS

**FIGURE 22**  
Transforming growth factor  $\beta$  receptor type II (TGF- $\beta$ -R)



**Fig. 23**

z21887\_p6(t7).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:TGR2\_HUMAN

Sequence documentation:

TGF-beta receptor type II precursor (EC 2.7.1.37) (TGFR-2) (TGF-beta type II receptor). Homo sapiens (Human). P37173; Q99474;

Alignment of: Z21887\_P6 x TGR2\_HUMAN ..

```

      1 MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQL 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQL 50

     51 CKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETV 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
     51 CKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETV 100

    101 CHDPKLPYHDFILEDAAAPKCIMKEKKKPGETFFMCSCSSDECNDNIIFS 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
    101 CHDPKLPYHDFILEDAAAPKCIMKEKKKPGETFFMCSCSSDECNDNIIFS 150

    151 EGEFSSLKGVGPEICANFLYPWSAVS                                176
      |
    151 E.....                                151
```

TGR2 structure

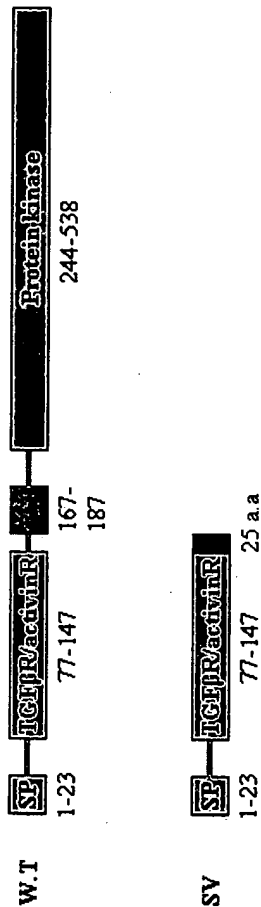


Fig. 24

**Fig. 25a**

**ITAV\_T3** (SEQ ID NO: 35)

gataaaaagcttttctcatttttaaaacaacagtcgcacggaagttcccgccgggacaaggg  
gaacgtgggtgcccttgctactcccgtggacgcggttagattgggacgctggaccgtatc  
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cccagcctcagacgctgctggagcgggcgagccggagggaagcaaaggaccgtctgcgc  
tgctgtccccgccccgcgcgtctgcgccccctcgtccctggcggtcgtccgaagctcag  
ccctcttgcttgcctgccccggagctgtcccgggttagccgagaagagagcgccggcgaagttt  
ggcgcgcgccagggcgggcgggcgccgctggcgccctcgtggggcgggggagggtgg  
ctaccgctcccggcttggtgctcccgcgcgccacttcggcgATCgcttttccgcccggcgga  
cggctgcgccctcgggtccccgcgggcctcccgtctcttctctcgggactcctgctacctctg  
tgccgcgccttcaacctagacgtggacagctcctgccagtagctctggccccgagggaagt  
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aaatgtgactgggtcttctaccgcgggtgccagccaattgaatttgatgcaacaggcaat  
agagattatgccaaggatgatccattggaatttaagtcccatcagtggtttggagcatct  
gtgaggtcgaaacaggataaaaattttggcctgtgccccattgtaccattggagaactgag  
atgaaacaggagcgagagcctgttggaacatgctttcttcaagatggaacaaagactgtt  
gagtatgctccatgtagatcacaagatattgatgctgatggacagggattttgtcaagga  
ggattcagcattgattttactaaagctgacagagtagcttcttggtgggtcctggtagcttt  
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attgcaattgctgctccatattgggggtgaagataaaaaaggaattgtttatatcttcaat  
ggaagatcaacaggcttgaacgcagtcctcatctcaaatcctgaagggcagtggtgct  
cgaagcatgccaccaagctttgggtatttcaatgaaaggagccacagatatagacaaaaat  
ggatatccagacttaattgtaggagctttttgggtgtagatcgagctatcttatacagggcc  
agaccagttatcactgtaaatgctgggtcttgaagtgtaccctagcattttaaatcaagac  
aataaaacctgctcactgcctggaacagctctcaaagtttcctgttttaagtgttaggtc  
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tccccaggtcactccaagaacatgactatttcaagggggggactgatgcagtgtaggaa  
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gaagacaatgtctgtaaacccaagctggaagtttctgtagatagtgatcaaaagaagatc  
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gagaggaacaactaagctactttaaaaaaaattctatgtaatttttatgtaaaactcta  
cattgggttaagtagtgctcagagatttcttgaatattttccctatacataaattcattt  
ttatttgacaaatagacttgtttaataaagcagtttatataatttgttgtttaaaataa  
attagttctacttgaataa

**Fig. 25b**

**ITAV\_T3 (SEQ ID NO: 33)**

MAFP PRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPA EYSGPEG SYFGFAVDFFVPSA  
SSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPIEF DATGNRDYAKDDPLEFKS  
HQWFGASVR SKQDKILACAPLYHWRTEMKQEREPVGT CFLQDGTKTVEYAPCRSQDIDAD  
GQGFCQGGFSIDFTKADRVLLGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYNNQLAT  
RTAQAI FDDSYLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE  
QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGDFQTTK  
LNGFEVFARFGSAIAPLGDDLQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQI  
LEGQWAARSMPPSFGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRARPVITVNAGLEVY  
PSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGVLPRKLN FQVELLLDKLKQKGAIRR  
ALFLYSRSPSHSKNMTISRGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD  
TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVDS DQKKIYIGDDNPLTLIVK  
AQNQGE GAYEAELIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQVCDLGNPMKAG  
TQLLAGLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSPV VSHKVDLAVLA AVEIRGVSSP  
DHIFLPIPNWEHKENPETEEDVGPVVQHIYEVCSC

## Integrin alpha-V

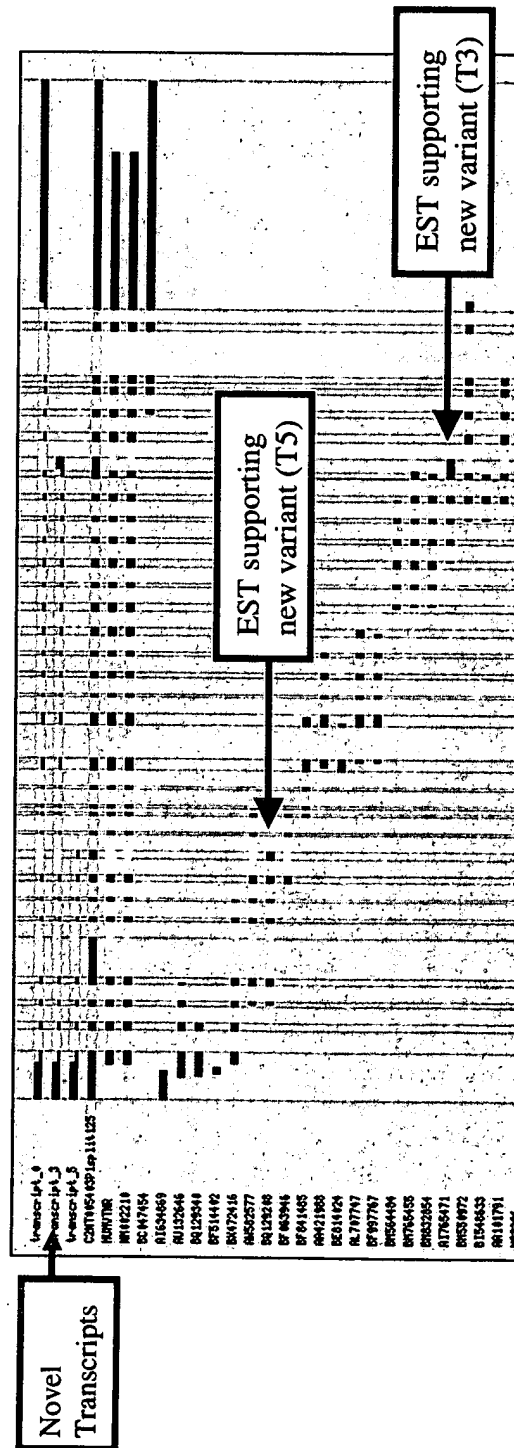


Fig. 27 (page 1/2)

humvtnr\_p3(t3).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:ITAV\_HUMAN

Sequence documentation:

Integrin alpha-V precursor (Vitronectin receptor alpha subunit) (CD51 antigen). Homo sapiens (Human). P06756;

Alignment of: HUMVTNR\_P3 x ITAV\_HUMAN ..

```

      1 MAFPPRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPAEGSYFG 50
      ||||||||||||||||||||||||||||||||||||||||
      1 MAFPPRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPAEGSYFG 50

    51 FAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPI 100
      ||||||||||||||||||||||||||||||||||||||||
    51 FAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPI 100

   101 EFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQ 150
      ||||||||||||||||||||||||||||||||||||||||
   101 EFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQ 150

   151 EREPVGTCFLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVL 200
      ||||||||||||||||||||||||||||||||||||||||
   151 EREPVGTCFLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVL 200

   201 LGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYNNQLATRQAIFDDS 250
      ||||||||||||||||||||||||||||||||||||||||
   201 LGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYNNQLATRQAIFDDS 250

   251 YLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE 300
      ||||||||||||||||||||||||||||||||||||||||
   251 YLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE 300

   301 QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSQGLQEVGQVSVSLQ 350
      ||||||||||||||||||||||||||||||||||||||||
   301 QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSQGLQEVGQVSVSLQ 350

   351 RASGDFQTTKLNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKK 400
      ||||||||||||||||||||||||||||||||||||||||
   351 RASGDFQTTKLNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKK 400

   401 GIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSFGYSMKGATDIDKNGYP 450
      ||||||||||||||||||||||||||||||||||||||||
   401 GIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSFGYSMKGATDIDKNGYP 450

   451 DLIVGAFGVDRAILYRARPVITVNAGLEVYPSILNQDNKTCSLPGTALKV 500
      ||||||||||||||||||||||||||||||||||||||||
   451 DLIVGAFGVDRAILYRARPVITVNAGLEVYPSILNQDNKTCSLPGTALKV 500

   501 SCFNVRFLKADGKGVLPKLNQVVELLLDKLKQKGAIRRALFLYSRSPS 550
      ||||||||||||||||||||||||||||||||||||||||
   501 SCFNVRFLKADGKGVLPKLNQVVELLLDKLKQKGAIRRALFLYSRSPS 550

   551 HSKNMTISRGGMLQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD 600
      ||||||||||||||||||||||||||||||||||||||||
   551 HSKNMTISRGGMLQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD 600
```



Fig. 27 (page 2/2)

```
601 TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVDSDQKKIYIG 650
    ||||||||||||||||||||||||||||||||||||||||||||||||
601 TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVDSDQKKIYIG 650

651 DDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEALARLSCAF 700
    ||||||||||||||||||||||||||||||||||||||||||||||||
651 DDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEALARLSCAF 700

701 KTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSS 750
    ||||||||||||||||||||||||||||||||||||||||||||||||
701 KTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSS 750

751 NLFDKVSPVVS HKVDLAVLA AVEIRGVSSPDHIFLPIPNWEHKENPETEE 800
    ||||||||||||||||||||||||||||||||||||||||||||||||
751 NLFDKVSPVVS HKVDLAVLA AVEIRGVSSPDHIFLPIPNWEHKENPETEE 800

801 DVGPPVQHIYEVCSC 815
    |||||||||
801 DVGPPVQHIYE.... 811
```

# ITAV structure

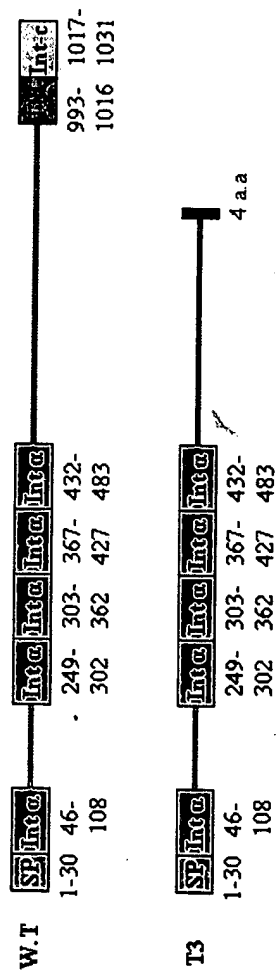


Fig. 28

**Fig. 29a**

**IL-10-R- $\beta$ \_T1 (SEQ ID NO: 39)**

ccccccatctccgctgggttcccggaagccgcgcgggacaagctctcccgggcgcgggcg  
ggggtcgtgtgcttggaggaagccgcggaacccccagcgccggtccATGgcgtggagcct  
tgggagctggctgggtggctgctgctggtgtcagcattgggaatggtagcacctccga  
aaatgtcagaatgaattctgttaatttcaagaacattctacagtgggagtcacctgcttt  
tgccaaaggggaacctgactttcacagctcagtaacctaatgttataggatattccaagataa  
atgcatgaatactaccttgacggaatgtgattttctcaagtctttccaagtatggtgacca  
caccttgagagtcagggctgaatttgcagatgagcattcagactgggtaaacatcacctt  
ctgtcctgtggatgacaccattattggacccccctggaatgcaagtagaagtacttgctga  
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gaagaatgtgtataactcatggacttataatgtgcaatactggaaaaacggtagctgatga  
aaagtttcaaattactccccagtatgactttgaggtcctcagaaacctggagccatggac  
aacttattgtgttcaagttcgaggggtttcttcctgatcggaacaaagctggggaatggag  
tgagcctgtctgtgagcaaacacccatgaCGtttttgggccatcctcatcaTAAacac  
ttctgtttttctcctttccattgtcggtgagaatgatgtttttgacaagctaagtgtca  
ttgcagaagactctgagagcgggaagcagaatcctggtgacagctgcagcctcgggaccc  
cgcttgggcagggggcccaagctaggctctgagaaggaaacacactcggctgggcacag  
tgacgtactccatctcacatctgcctcagtgaggatcagggcagcaacaagggccaag  
accatctgagccagcccccacatctagaactccagacctggacttagccaccagagagc  
tacattttaaggctgtcttggcaaaaatactccatttgggaactcactgccttataaag  
gctttcatgatgttttcagaagttggccactgagagtgtaattttcagccttttatatca  
ctaaaataagatcatgttttaattgtgagaaacagggccgagcacagtggctcacgcctg  
taataccagcaccttagaggtcgagggcaggcggatcacttgaggtcaggagttcaagacc  
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tggtatggactgatctgaaaatcaacctcaactcaaggggtggtcagctcaatgctacacag  
agcacggacttttggattctttgcagtaactttgaattttttttctacctatatatgttt  
tatatgctgctggtgctccattaaagttttactctgtgttgactatatgtgttcatgat  
aaaaaa

**Fig. 29b**

**IL-10-R- $\beta$ \_T1 (SEQ ID NO: 37)**

MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYR  
IFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQV  
EVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRN  
LEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDVFGPSSS

## FIGURE 30



**Fig. 31**

t48767\_p2(t1).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:I10S\_HUMAN

Sequence documentation:

Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)  
(Cytokine receptor class-II CRF2-4). Homo sapiens (Human). Q08334;

Alignment of: T48767\_P2 x I10S\_HUMAN ..

```

      1 MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPFAKGNL 50
      ||||||||||||||||||||||||||||||||||||||||||||
      1 MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPFAKGNL 50

     51 TFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDW 100
      ||||||||||||||||||||||||||||||||||||||||||||
     51 TFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDW 100

    101 VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYN 150
      ||||||||||||||||||||||||||||||||||||||||||||
    101 VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYN 150

    151 SWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCVQVRGFLPDRNK 200
      ||||||||||||||||||||||||||||||||||||||||||||
    151 SWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCVQVRGFLPDRNK 200

    201 AGEWSEPVCETTHDVFGPSSS                                222
      ||||||||||||||||
    201 AGEWSEPVCETTHD.....                                215
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# IL10- R- $\beta$ chain structure

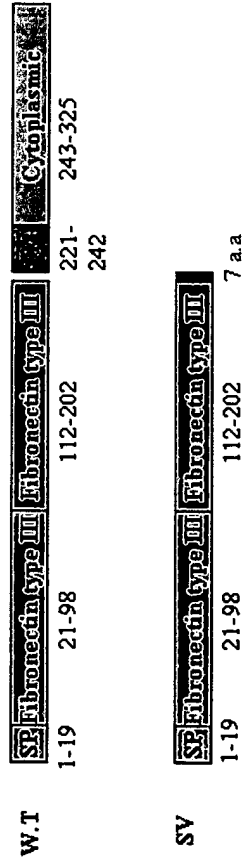


Fig. 32

**Fig. 33a**

**INR1\_T11** (SEQ ID NO: 43)

agaagagggcgcgctgctgtagagggcggtgagagctaagaggggcagcgctgtgcag  
agggcggtgtgacttaggacggggcgatggcggtgagaggagctgcgcgtgcgcgaac  
atgtaactgggtgggatctgcggcggtcccgatgATGgtcgtcctcctgggcgcgacga  
ccctagtgtcgtcgccgtggcgccatgggtgttgtccgcagccgcaggtggaaaaatc  
taaaatctcctcaaaaagtagaggtcgacatcatagatgacaactttatcctgaggtgga  
acaggagcgatgagtcgtcggaatgtgactttttcattcgattatcaaaaaactggga  
tggaataattggataaaattgtctgggtgtcagaatattactagtaccaaagtcaactttt  
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acacttcttcatggatgaggttgactcatttacaccatttcgcaaagctcagattggtc  
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ccatggatgaaaagctgaataaaaagcagtggttttttagtgacgctgtatgtgagaaaacaa  
aaccaggtcagaatcttttattgtcttttttaaaaatgTAGctagacataataaaagtaa  
ttctatactgta



**Fig. 33b**

**INR1\_T11** (SEQ ID NO: 41)

MVLLGATTLVLVAVAPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTF  
SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDST  
PFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLVIWKNSSGVEERIE  
NIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN  
QNYVLKWDYTYANMTFQVQWLHAFLKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKG  
IYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPV  
IQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVF  
SDAVCEKTKPGQNLLLSFLKM

**FIGURE 34**

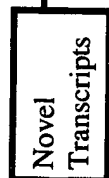


Fig. 35

t07758\_p5(t11).pfs

Sequence name: /dir/tp/CGC/DATA/analysis\_db/sw.fasta:INR1\_HUMAN

Sequence documentation:

Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
Homo sapiens (Human). P17181;

Alignment of: T07758\_P5 x INR1\_HUMAN ..

```

1 MVVLLGATTTLVLVAVAPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW 48
  |||||
2 MVVLLGATTTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW 49

49 NRSDES VGNVTF SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVEE 98
  |||||
50 NRSDES VGNVTF SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVEE 99

99 IKLRIRAEKENTSSWYEVD SFTPF RKAQIGPPEVHLEAEDKAIVIHISPG 148
  |||||
100 IKLRIRAEKENTSSWYEVD SFTPF RKAQIGPPEVHLEAEDKAIVIHISPG 149

149 TKDSVMWALDGLSFTYSLVIWKNSSGVEER IENIYSRHKIYKLSPETTY 197
  |||||
150 TKDSVMWALDGLSFTYSLLIWKNSSGVEER IENIYSRHKIYKLSPETTY 198

198 CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW 247
  |||||
199 CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW 248

248 DYT YANMTFQVQWLHAF LKR NPGNHLYKWKQIPDCENVKTTQCVFPQNVF 297
  |||||
249 DYT YANMTFQVQWLHAF LKR NPGNHLYKWKQIPDCENVKTTQCVFPQNVF 298

298 QKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHI 347
  |||||
299 QKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHI 348

348 YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKII EKKT DVTVPNLKP 397
  |||||
349 YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKII EKKT DVTVPNLKP 398

398 LTVYCVKARAHTMDEKLNKSSVFS DAVCEKTKPGQNLLLSFLKM 441
  |||||
399 LTVYCVKARAHTMDEKLNKSSVFS DAVCEKTKPG..... 432
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# INR1 structure

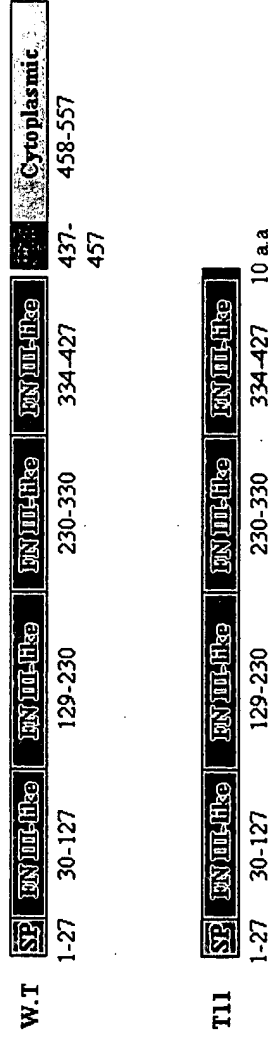


Fig. 36